PLANT ANIMAL INTERACTIONS

Larval settlement of the common Australian sea urchin *Heliocidaris erythrogramma* in response to bacteria from the surface of coralline algae

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Abstract Bacterial biofilms are increasingly seen as important for the successful settlement of marine invertebrate larvae. Here we tested the effects of biofilms on settlement of the sea urchin *Heliocidaris erythrogramma*. Larvae settled on many surfaces including various algal species, rocks, sand and shells. Settlement was reduced by autoclaving rocks and algae, and by treatment of algae with antibiotics. These results, and molecular and culture-based analyses, suggested that the bacterial community on plants was important for settlement. To test this, approximately 250 strains of bacteria were isolated from coralline algae, and larvae were exposed to single-strain biofilms. Many induced rates of settlement comparable to coralline algae. The genus *Pseudoalteromonas*

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Present Address: M. J. Huggett (⊠) Kewalo Marine Laboratory, University of Hawaii, 41 Ahui Street, Honolulu, HI 96813, USA e-mail: huggett@hawaii.edu dominated these highly inductive strains, with representatives from Vibrio, Shewanella, Photobacterium and Pseudomonas also responsible for a high settlement response. The settlement response to different bacteria was species specific, as low inducers were also dominated by species in the genera Pseudoalteromonas and Vibrio. We also, for the first time, assessed settlement of larvae in response to characterised, monospecific biofilms in the field. Larvae metamorphosed in higher numbers on an inducing biofilm, Pseudoalteromonas luteoviolacea, than on either a low-inducing biofilm, Pseudoalteromonas rubra, or an unfilmed control. We conclude that the bacterial community on the surface of coralline algae is important as a settlement cue for H. erythrogramma larvae. This study is also an example of the emerging integration of molecular microbiology and more traditional marine eukaryote ecology.

Introduction

Most benthic marine invertebrates have a complex life cycle involving a sessile, benthic adult phase, and a planktonic larval phase. The series of events whereby tiny larvae, weeks or months after fertilisation, are able to locate, settle and metamorphose in a habitat, where juveniles are then capable of successfully establishing themselves, is a key part of the life cycle of such organisms. This process is crucial to population and community dynamics, biogeography, gene flow, and macroevolution of marine invertebrates, and remains one of the central foci of marine research (Thorson 1950; Butman 1987; Caley et al. 1996; Pechenik 1999).

Settlement and recruitment of propagules are complex processes, determined by the interaction of biotic and abiotic factors that operate at different spatial and temporal scales (Rodriguez et al. 1993). At a large scale, a variety of hydrodynamic factors, e.g. flow (Abelson and Denny 1997), light and gravity (Kobak 2001) play important roles in settlement. Within a habitat, more environmentally specific factors become important (Butman 1987). Environmental cues including physical factors such as surface texture (Callow et al. 2002) and small-scale flow (Boxshall 2000), biological factors such as the presence of adult conspecifics (Zhao and Qian 2002) and chemical factors associated with various aspects of the habitat (Fusetani 1997) are thought to be most influential at small scales. Chemical cues in particular, from both natural and artificial sources, have received considerable attention in the literature (reviewed by Pawlik 1992; Steinberg and de Nys 2002). Compounds arising from plants (Morse et al. 1984; Morse 1992; Williamson et al. 2000), prey (Pawlik 1992), conspecifics (Burke 1984, 1986; Pawlik 1992), and biofilms (Johnson and Sutton 1994) can all act as settlement cues for larvae.

As early as 1935, Zobell and Allen (1935) noted that many marine invertebrate larvae require a bacterial biofilm to enable settlement to occur, and we now know that larvae from a number of phyla including echinoderms (Johnson et al. 1991b), cnidarians (Negri et al. 2001), polychaetes (Unabia and Hadfield 1999), gastropods (Rodriguez et al. 1995) and crustaceans (Neal and Yule 1994), settle in response to biofilms of either single or mixed bacterial communities (reviewed by Hadfield and Paul 2001). Factors such as the age of the biofilm (Keough and Raimondi 1995), origin of the biofilm (Johnson et al. 1991a), and whether or not the biofilm is presented in combination with another surface (Johnson and Sutton 1994; Negri et al. 2001) all mediate the response of settling larvae (reviewed by Wieczorek and Todd 1998; Holmström and Kjelleberg 2000). With respect to particular assemblages or taxa present in inducing biofilms, bacteria associated with coralline algae are important for settlement of a number of invertebrates such as the crown-of-thorns starfish (Johnson et al. 1991b; Johnson and Sutton 1994), corals and other cnidarians (Leitz 1997; Negri et al. 2001), and bacteria from the genus Pseudoalteromonas are common as mediators of larval settlement as inducers (Lau and Qian 2001; Negri et al. 2001) or inhibitors (Holmström et al. 1992; Holmström and Kjelleberg 2000).

Beyond these few observations, however, there are few generalities regarding the types of interactions that occur between settling invertebrate larvae and biofilms. One generalisation regarding the effect of biofilms on larval settlement was proposed by Steinberg et al. (2001). They suggested that larvae of generalist marine herbivores, i.e. those that feed on a wide range of host plants and are not associated with any particular plant species, respond to bacterial biofilms, while larvae of specialist marine herbivores, i.e. those that feed on a discrete range of plants, and are often small, mobile and live on their food source, respond to cues associated with their host plant. For specialist herbivores, there are now a number of examples of larvae that settle in response to compounds secreted by their host alga (Boettcher and Targett 1998; Krug and Manzi 1999; Williamson et al. 2000; Swanson et al. 2004). For generalists (Pearce and Scheibling 1991; Gosselin and Jangoux 1996; Lamare and Barker 2001), larvae may be responding to more broadly distributed cues, such as the bacterial biofilms associated generally with surfaces in shallow subtidal habitats.

A second gap that currently exists in biofilm/larval settlement studies is the linking together of laboratory and field studies. There are a number of laboratory studies that have focussed on bacterial cues as triggers for settlement and metamorphosis. Far fewer studies have been conducted in the field in an attempt to understand in situ larval responses (e.g. Keough and Raimondi 1995) and how the distribution and/or amount of various cues might actually influence larval settlement (Underwood and Keough 2000) and none of these have manipulated or characterised biofilm-derived cues except in a very general way (e.g. biofilm age). A clear challenge for the future is to develop reliable techniques, incorporating modern microbiological methods, to monitor and manipulate biogenic cues and rates of larval arrival in experiments under field conditions.

Here, the prediction that larvae of generalist herbivores will respond to biofilm-derived cues, rather than host plant cues, is explored using the generalist marine herbivore *Heliocidaris erythrogramma*. *H. erythrogramma* is an endemic Australian sea urchin found in coastal waters from 1.5 to 35 m depth. *H. erythrogramma* feeds on a wide range of sources including seagrasses, macroalgae, encrusting coralline algae (CCA) and diatoms (Keesing 2001), and currently supports a commercially important fishery. Despite being common and widespread within Australia (Keesing 2001), the ecology of *H. erythrogramma* is relatively unknown. Factors affecting the settlement and recruitment of this urchin have not previously been studied. Here we ask:

- 1. Does *H. erythrogramma* respond to host plants, or to associated biofilms?
- 2. If *H. erythrogramma* does respond to biofilms, are there specific bacterial strains that induce settlement, or are there many strains that cause the same response?

3. Do larvae of *H. erythrogramma* respond to characterised biofilms in the field?

Materials and methods

Culturing of larvae

Heliocidaris erythrogramma larvae were reared in filtered seawater (FSW) in aerated beakers at 19°C. After approximately 3 days larvae were competent (Williams and Anderson 1975) and a haphazard selection was used in assays.

Study organisms and study sites

Settlement assays were done using local substrata collected from Shark Bay (33°51′09″S, 151°16′00″E) and Bare Island (33°59′38″S, 151°14′00″E). The green alga *Ulvella lens* was also tested and was grown on plastic plates at Melbourne University, and maintained at the University of New South Wales (UNSW) at 19°C. *U. lens* induces settlement of the generalist herbivore *Haliotis rubra* (Daume et al. 2000) but was not found at local sites. Recruitment surveys and field experiments were done at Bare Island.

Protocol for settlement assays

Here we define "settlement" as the attachment of a larva to the substrate after metamorphosis. Pieces of algae (50 mg wet weight) were used for assays, with the exception of U. lens that was grown on plastic plates and cut into 1-cm² pieces and CCA, presented as a minimum of 95% cover on small rocks $\sim 1 \text{ cm}^2$. Small rocks and shells as well as sand and shell grit were also used. Each replicate piece of alga, rock or square of plate was selected from a new plant, rock or plate. Assays had ten replicates of each treatment including FSW controls. Algal pieces and five competent larvae were added to sterile 5-ml Petri dishes containing FSW, except for the first algal assay, where only one larva per dish was added, and the initial assay (see Culturing of larvae) testing for gregarious settlement. After 48 h the number of settled individuals per dish was counted using a dissecting microscope and recorded.

Gregarious settlement

To determine if competent larvae respond gregariously to conspecifics, an assay was conducted with densities of 1, 5, 10 and 50 larvae per dish. Positive controls of CCA were included for each density. Settlement in response to algae and biofilmed (but otherwise non-living) surfaces

Dictyota dichotoma, Ecklonia radiata, Dilophus marginatus, Sargassum vestitum, Sargassum linearfolium, Delisea pulchra, two species of geniculate coralline algae, Corallina officinalis and Amphiroa anceps, mixed unidentified CCA, Gracilaria sp., Homeostrichus sp., Codium fragile, Caulerpa filiformis, Enteromorpha sp., Ulva australis, and Ulva lens were used to assess the settlement response of larvae to algae from the adult habitat. To assess larval response to biofilmed (but otherwise non-living) surfaces, sand, shell, shell grit and rocks were collected from Shark Bay, in the vicinity of adult H. erythrogramma. C. officinalis was used as a positive control.

Settlement in response to sterile rocks and A. anceps

Larvae settled broadly in response to various surfaces, suggesting a common, broadly distributed cue. To determine if this cue was associated with bacterial bio-films, 20 rocks were collected from Bare Island. Ten of these were scrubbed and autoclaved to remove the surface biofilm. Twenty pieces of *A. anceps* were also collected and ten pieces were autoclaved (but not scrubbed, so as to present the plants intact). The remainder were used as controls.

Controls for effect of antibiotics

The results from Settlement in response to sterile rocks and *Amphiroa anceps* suggested that biofilms could be important as settlement cues. We then conducted a series of experiments aimed at separating the effect of the algae or non-living surfaces (on settlement) from that of their biofilms. Prior to commencing these assays, the effect of antibiotics was assessed.

To test the effects of antibiotics against larvae, a batch was divided into two cultures immediately following fertilisation. One was reared in FSW containing antibiotics (20 mg/l streptomycin sulphate, 10 mg/l penicillin G, 2 mg/l neomycin sulphate and 10 mg/l kanamycin sulphate) and the other in FSW only. An assay was conducted with five larvae from each treatment with either *C. officinalis* or FSW only.

To test the effects of antibiotics on settlement to a known chemical cue, *H. erythrogramma* larvae were exposed to histamine, which induces settlement in some species of sea urchins (Swanson et al. 2004). Treatments were histamine with antibiotics (same concentrations as above) and histamine alone. FSW and *A. anceps* were used as controls.

To test the effects of antibiotics on a cue produced by a plant, the red alga *D. pulchra* was used. *D. pulchra* produces a chemical cue (histamine) that rapidly induces settlement of the sea urchin, *Holopneustes purpurascens* (Swanson et al. 2004). Pieces of *D. pulchra* were submitted to one of the following five treatments, and exposed to larvae.

Antibiotic treatment

Algae were soaked in a 10% Betadine solution in FSW for 5 min, rinsed, then soaked in FSW containing streptomycin sulphate (20 mg/l), penicillin G (10 mg/l), neomycin sulphate (2 mg/l) and kanamycin (10 mg/l) for 48 h (modified from Xue-wu and Gordon 1987; Johnson and Sutton 1994). Algae were rinsed before addition to assay dishes.

Antibiotic treatment with agar wipe

Identical to Antibiotic treatment with the addition of wiping algae over the surface of sterile agar both before soaking in Betadine and after soaking in the antibiotic solution. This treatment was included in order to facilitate the physical removal of the biofilm from the surface of the algae.

Control treatment for the agar wipe process

The plant was wiped over the surface of sterile agar and gently rinsed in FSW.

Control treatment for soaking

Algal pieces were soaked in FSW for 48 h.

Unmanipulated control

A piece of algae.

Bacterial community characterisation

To determine the effect of the antibiotic treatments in removing bacteria from the algal surfaces, the number and diversity of bacteria on each of the treatments was first assessed using culturing methods. *C. officinalis* and *A. anceps* were treated with the same five treatments listed in Controls for effect of antibiotics. Triplicate pieces of each were added to 1 ml FSW, vortexed then serially diluted to 10^{-4} . One hundred microlitres of each dilution was spread evenly onto Marine Agar 2216 plates. Plates were observed daily for 2 weeks, and the number and diversity of colonies per plate counted (Prescott et al. 1995).

To further assess the affect of antibiotic treatments on the microbial community diversity of plants treated with antibiotics, a DNA fingerprinting technique, denaturing gradient gel electrophoresis (DGGE), was done. For each antibiotic treatment, five replicate samples of *C. officinalis* and *A. anceps* were prepared via DNA extraction and polymerase chain reaction (PCR), and run on a BioRad Dcode system following the methods of Dahllöf et al. (2000). DGGE gels were run using the rpoB gene, rather than 16S rDNA as it is known to produce a single band per bacterial species, while 16S rDNA primers can yield up to four bands per species, biasing community analyses (Dahllöf et al. 2000). Three representative samples of each treatment were selected for DGGE analysis.

Antibiotic assays

The above experiments established that antibiotics did not affect a known plant cue and had no apparent direct effect on larval settlement. We then used these techniques to assess whether *H. erythrogramma* larvae responded to a cue emitted by the plant itself, or to the biofilm on the algal surface. The experiment was done using *H. erythrogramma* larvae and the two coralline algal species *A. anceps* and *C. officinalis*, which were subjected to the treatments described in Controls for effect of antibiotics.

Settlement in response to single-strain bacterial films

Each bacterial morphotype cultured as described in this section was re-streaked until purity and stored in 30% glycerol at -80° C. Approximately 125 strains were isolated from *C. officinalis* and a further 125 from *A. anceps*. From these, single-strain biofilms were created by placing five sterile coverslips in 10 ml marine broth inoculated with a single strain. Cultures were grown overnight, allowing biofilms to form on the coverslips. These were then gently rinsed and used in a series of settlement assays (method adapted from Negri et al. 2001).

To determine if any particular phylogenetic group of bacteria were responsible for approximately 70 strains, 35 that induced high settlement, and a further 35 that induced low settlement, were sequenced. Isolates were grown overnight in Marine Broth 2216, spun, and the pellet retained. The DNA extraction procedure was identical to that for the whole community analysis. The 16S rDNA primers used were F27 (5'-GAGTT TGATCCTGGCTCAG-3') and R1492 (5'-ACGGTT ACCTTGTTACGACTT-3'). One hundred nanograms DNA was added to a 17 μ l PCR mixture with 2 μ l Sigma REDtaq buffer, 2.5 mM each DNTP, 5 pmol of each primer, 3.2 μ g BSA and sterile milliQ water. The PCR conditions were 94°C for 3 min, then 25 cycles each of 1 min at 94°C, 1 min at 55°C, and 2 min at 72°C. A final extension step of 72°C for 5 min was then performed. Purified PCR product (~ 100 ng) was sequenced unidirectionally using BigDye terminator cycle sequencing reaction mix (Applied Biosystems), with either F27, R1492 or 530F (5'-GT GCCAGCMGCCGCGG-3'), then analysed on an ABI 310 DNA sequencing system. Sequences were analysed using the BLAST search algorithm (Altschul et al. 1990) available through the National Centre for Biotechnology Information website (http://www.ncbi. nlm.nih.gov).

Larval traps—monitoring recruitment to high- and low-inducing biofilms

Recruitment of *H. erythrogramma* to biofilms was monitored using larval traps from November 2003 until March 2004 at Bare Island, Botany Bay. Traps were made of PVC piping with a rectangular window in the top and lined with Astroturf. Traps were filmed with either the high inducer, *Pseudoalteromonas luteoviolacea* (strain A316, see below) or the low inducer, *Pseudoalteromonas rubra* (strain C312, see below), or used as unfilmed controls. Each week, ten replicates of each treatment were randomly assigned to holders (n = 30) secured to the rocky reef at 3 m depth, left in the field, then collected, sealed underwater and replaced with freshly filmed traps. At UNSW traps were examined for recruits.

Traps were sampled to verify the persistence of the biofilm that was incubated inside them. Triplicate swabs were taken from inside three of each treatment at the end of incubation and from three more of each after 48 h in the field. Swabs were wiped over the surface of marine agar plates, and the number and diversity of colonies that grew were recorded. To verify that the purple pigmented colonies were strain A312 (*P. luteoviolacea*), and that the red pigmented colonies were pigmented strain C312 (*P. rubra*), four colonies of each colour were selected from plates and sequenced as described above.

There was no natural recruitment of *H. erythro*gramma to traps. In order to overcome this, larvae were cultured then released in the field. Ten replicates of each trap treatment were prepared, filled with FSW and approximately 150 larvae added to each. A piece of 100-µm mesh was fitted across the window and secured in place with rubber bands, forcing larvae to remain inside the trap. Traps were left in the field for 48 h, collected and examined at UNSW. A second experiment tested the ability of larvae to detect, locate and recruit to biofilms in the field. Ten replicates of each treatment were deployed and approximately 250 larvae were gently syringed into the water adjacent to (< 10 cm) each trap. After 24 h traps were collected and examined at UNSW.

Data analysis

All settlement assays were analysed using SYSTAT (Wilkinson 1997). Data for ANOVAs were checked for normality and heterogeneity of variance using frequency histograms of residuals and plots of residuals versus means, respectively. Arcsin square root transformations were performed where appropriate. Assays that used only one larva per dish were analysed using Pearsons χ^2 . Single larva data for the gregarious settlement assay were excluded from the analysis. Post-hoc tests (Tukey's multiple range) were performed where appropriate. Differences in bacterial community composition on seaweeds were analysed using non-metric multidimensional scaling (MDS) and analysis of similarities (ANOSIM) (Clarke and Warwick 1994). Following MDS a one-way ANOSIM was conducted with seaweed as the factor.

Results

Gregarious settlement

There was no evidence of gregarious settlement by *H.* erythrogramma larvae. When larvae were alone in assay dishes, six out of ten settled in response to CCA. This was comparable to higher density treatments $(47 \pm 7, 45 \pm 5 \text{ and } 46 \pm 10\%; n = 5, 10 \text{ and } 50 \text{ larvae},$ respectively). Larval settlement also did not increase with increasing density when in the presence of CCA in the dishes (one-factor ANOVA, $F_{2,27} = 0.226$, P = 0.779, data arcsin transformed). In sterile seawater alone, no settlement occurred at any density.

Settlement in response to algae and biofilmed (but otherwise non-living) surfaces

Larvae settled in response to most algae tested, although settlement rates varied. Larvae responded most strongly to coralline algae. Three assays were conducted, and the result of one representative assay is given in Fig. 1a ($\chi^2 = 1, P < 0.05, df = 5$). Over the three assays settlement in response to the coralline red algae *A. anceps, C. officinalis* and CCA, the brown alga *S. linearifolium*, and the green alga *C. fragile* was

consistently high. The brown alga *E. radiata*, the green algae *U. australis* and the red alga *D. pulchra* only induced low rates of settlement. No settlement was observed in FSW alone.

Larvae settled in response to all biofilmed surfaces (Fig. 1b, $F_{6,63} = 15.649$; P < 0.05). However, the positive control, *C. officinalis*, induced a much higher rate of settlement (94 ± 3%) than rocks (58 ± 9%), sand (50 ± 11%), shell grit (46 ± 10%) and shell (46 ± 14%). All surfaces induced higher rates of settlement than seawater collected from the adult habitat (0 ± 0%) and FSW (10 ± 8%).

Settlement in response to sterile and filmed rocks and algae

"Sterilisation" via autoclaving and, for rocks, scrubbing and autoclaving, reduced settlement on both rocks and



Fig. 1 *Heliocidaris erythrogramma* larval settlement after 48 h in response to **a** local algal species, and **b** biofilmed (but otherwise non-living) surfaces. Data for **a** are proportion of larvae settled, n = 10, and **b** mean percent settlement \pm SE, n = 10. *Aa Amphiroa anceps, Co Corallina officinalis, Sl Sargassum linearfolium, Cf Codium fragile, Sv Sargassum vestitum, Er Ecklonia radiata, Dp Delisea pulchra, R rock, S sand, Sh shell, Sg shell grit, FSW filtered seawater, SW seawater collected from the adult habitat*

A. anceps (Fig. 2, $F_{4,45} = 17.996$; P < 0.01). Settlement in response to "sterile" substrata did not differ from that for FSW.

Effect of antibiotics on larvae

Settlement was not affected by the addition of antibiotics to assay dishes (Fig. 3a) as settlement remained high (between 88 ± 64 and $86 \pm 5\%$) for all larvae presented with *C. officinalis* despite being exposed to antibiotics (Fig. 3a, $F_{3,36} = 135.74$; P < 0.01).

Effect of antibiotics

H. erythrogramma larvae settled at the same rate in response to histamine, even when antibiotics were included in dishes (Fig. 3b).

Settlement of *Holopneustes purpurascens* was not affected by the addition of antibiotics to *D. pulchra* (Fig. 4, $F_{4,45} = 1.103$; P = 0.366). This assay indicates that a known chemical cue arising from a plant was not affected by the antibiotic treatments applied to it. We thus proceeded to extend this treatment to *A. anceps* and *C. officinalis*, the coralline algae that induced settlement of *H. erythrogramma*.

Bacterial abundance and diversity

For both *A. anceps* and *C. officinalis*, the abundance of culturable bacteria was not reduced in the presence of antibiotics, but bacterial diversity was, thus altering the microbial community on the surface of plants (Table 1). The abundance of bacteria actually



Fig. 2 *H. erythrogramma* larval settlement in response to "sterile" rocks and algae. Data are mean percent settlement \pm SE, n = 10. (*A*) Rock or alga was autoclaved; for other abbreviations, see Fig. 1



Treatment. Corallina = Corallina officinalis. AB indicates antibiotics were added to assay



Fig. 3a, b Effect of antibiotics on larvae and on a known chemical settlement cue. **a** *H. erythrogramma* larval settlement after rearing in antibiotics. **b** *H. erythrogramma* larval settlement to histamine (*H*) in the presence (*A*) and absence of antibiotics. Aa was the positive control. For other abbreviations, see Fig. 1

increased on *A. anceps* treated with antibiotics compared to controls. This increase was reduced to natural levels by the agar wipe (Table 1, $F_{4,10} = 7.278$; P < 0.01). A similar trend was observed for *C. officinalis*



Fig. 4 Holopneustes purpurascens settlement in response to Delisea pulchra treated with antibiotics. Data are mean percent settlement \pm SE, n = 10. C Unmanipulated control, S soaking control, W wiping control, AW antibiotic treatment plus wipe, AB antibiotic treatment

(Table 1, $F_{4,10} = 9.938$, P = 0.35). For *A. anceps* treated with antibiotics, the diversity of bacteria was much less than for control plants (Table 1, $F_{4,10} = 15.159$, P < 0.01). A similar trend was observed for *C. officinalis* (Table 1, $F_{4,10} = 3.480$; P = 0.064).

Molecular analysis also showed that bacterial communities associated with *C. officinalis* and *A. anceps* changed in the presence of antibiotics (*A. anceps*, R = 0.558, significance level 0.1%; *C. officinalis*, R = 0.343, significance level 0.3%). Patterns were very similar for both algal species and representative *A. anceps*; figures are shown (Fig. 5). For *A. anceps*, bacterial community composition was > 78% similarity within control and unmanipulated plants, whereas

Table 1 Cultured bacterial abundance and diversity on *Amphiroa anceps*^a and *Corallina officinalis*^b after treatment with antibiotics. Data are mean numbers per 0.1 g wet weight algae \pm SE,

n = 3. Letters in parentheses indicate results of one-way ANO-VAs. Data that share a letter do not differ statistically. *FSW* Filtered seawater

Seaweed	Treatment	Diversity (number of colonies per 0.1 g algae \pm SE)	Abundance (number of bacteria $\times 10^5$ per 0.1 g algae \pm SE)
A. anceps	Soaking control	35.67 ± 3.56 (a)	57.33 ± 0.01 (a)
A. anceps	Unmanipulated control	21.33 ± 3.89 (b)	1.17 ± 0.01 (a)
A. anceps	Agar wipe control	13.33 ± 6.18 (bc)	1.19 ± 0.33 (a)
A. anceps	Antibiotics	10.67 ± 0.71 (c)	357.78 ± 0.01 (b)
A. anceps	Antibiotics + agar wipe	5 ± 1.78 (c)	177 ± 0.59 (ab)
C. officinalis	Soaking control	18.67 ± 7.97	$2,082.22 \pm 1731.26$ (a)
C. officinalis	Unmanipulated control	16.33 ± 1.33	39.18 ± 29.88 (abc)
C. officinalis	Agar wipe control	9.33 ± 2.40	3.71 ± 2.12 (bc)
C. officinalis	Antibiotics	3.33 ± 0.33	888.89 ± 528.09 (ab)
C. officinalis	Antibiotics + agar wipe	6.33 ± 0.88	51.56 ± 9.75 (ab)
FSW	_	1.33 ± 0.88	0.01 ± 0.01

^a A. anceps abundance, $F_{4,10} = 7.278$, P < 0.01; diversity, $F_{4,10} = 15.159$, P < 0.01

^b Data for *C. officinalis* were log transformed. *C. officinalis* abundance, $F_{4,10} = 9.938$, P < 0.05; diversity, $F_{4,10} = 3.480$, P = 0.064

those plants treated with antibiotics had < 65% similarity to controls, and most had < 60% similarity (Fig. 5b). For *C. officinalis* all plants treated with antibiotics shared < 70% similarity to controls and unmanipulated plants, with half of these sharing < 50% similarity to control. Bacterial community diversity within control and unmanipulated plants generally shared at least 75% similarity.

Effect of antibiotics on settlement of H. erythrogramma

Settlement in response to both *A. anceps* and *C. officinalis* was significantly reduced in the presence of antibiotics ($F_{4,45} = 13.047$, P < 0.001 and $F_{4,45} = 17.063$, P < 0.01, Fig. 6). Unmanipulated plants and controls all induced a high rate of settlement. Settlement in response to single-strain biofilms

Settlement of *H. erythrogramma* on bacterial strains was varied (see Fig. 7). Many strains induced a high settlement response, similar to the coralline algal control. FSW consistently produced negligible settlement and many bacterial strains induced low or no settlement.

Bacteria inducing a high rate of settlement were dominated by the genus *Pseudoalteromonas* (Table 2). *Pseudoalteromonas*, *Vibrio*, *Shewanella*, *Photobacterium* and *Alphaproteobacteria* were present in both the high- and low-inductive groups. Other strains that induced high rates of larval settlement included *Alteromonas*, *Aestueariibacter*, *Cytophaga*, *Micrococcus*, *Thalassomonas* and *Pseudomonas*. *Roseobacter*,



Fig. 5a, b Bacterial community composition of *A. anceps* treated with antibiotics. **a** *rpoB* denaturing gradient gel electrophoresis gel, showing banding patterns across three replicates within each

treatment. **b** Cluster diagram representing the presence or absence of bands in **a**. For abbreviations, see Fig. 4. *M* marker lane



Fig. 6 *H. erythrogramma* larval settlement in response to **a** *A. anceps* and **b** *C. officinalis*, treated with antibiotics. Data are mean percent settlement \pm SE. For abbreviations, see Fig. 4

Paracoccus, Ferrimonas, Algoriphagus and *Ruegaria* were present only among the low inducers.

Counts of bacteria in traps deployed in the field

For both the high and low inducer, biofilms in traps remained dominated by the strain they were inoculated with after 48 h in the field. For traps filmed with *P. luteoviolacea*, a mean of 97.97 \pm 1.3% cover was found, and for traps filmed with *P. rubra* a mean of 98.08 \pm 1.2% cover was found. Control traps appear to have been slightly contaminated with both *P. luteoviolacea* and *P. rubra*: after forty-eight hours 14.7 \pm 6.9% of cells were *P. luteoviolacea* and 0.16 \pm 0.16% of cells found in traps were *P. rubra*. This contamination did not result in higher numbers of recruits into traps. For *P. luteoviolacea* and *P. rubra* the three haphazardly selected pigmented colonies matched 100% with the strain they were inoculated with, for > 1,350 bp, validating the culture counts. Larval traps—monitoring recruitment to high- and low-inducing biofilms

No *H. erythrogramma* larvae were found in any traps, despite traps being in the field for several months during the adult spawning period.

Larval release to traps filmed with high and low inducers

Significantly more larvae metamorphosed in response to high inducers in enclosed traps in the field than to either the unfilmed or filmed control (Fig. 8, $F_{2,27} = 20.69$, P < 0.001). Furthermore, larvae released near traps recruited to traps filmed with the high inducer more than to traps filmed with the low inducer or the unfilmed control ($F_{2,27} = 3.354$, P = 0.054). This result was not significant as recruitment was very low, with a mean of only 7.1 \pm 1.8 urchins recruiting to traps filmed with the high inducer.

Discussion

There is a growing body of evidence that suggests that generalist herbivores have broad patterns of settlement. Urchin examples include Evichinus chloroticus, which settles in response to rocks, shells, coralline algae and biofilms (Lamare and Barker 2001), Paracentrotus lividus which settles in response to algae, and detritus particles (Gosselin and Jangoux 1996) and Strongylocentrotus droebachiensis which settles in response to various red and brown macroalgae, filmed cobbles and biofilms (Pearce and Scheibling 1991). Abalone also settle in response to a suite of stimuli including macroalgae (Daume et al. 2000), diatoms (Gordon et al. 2004), mucus trails (Gallardo and Buen 2003) and coralline algae (Daume et al. 1999). H. erythrogramma also exhibits high settlement in response to a range of macroalgae and biofilmed surfaces. The response of these larvae of generalist herbivores to a range of stimuli indicates that either: (1) larvae are responding to a variety of different types of cues, or (2) larvae are responding to one cue that is shared by all of these stimuli. Conversely, specialist marine herbivores with narrow host ranges often settle specifically in response to host-derived cues. For example Alderia modesta, metamorphoses exclusively in response to the obligate adult food, the green alga Vaucheria longicaulis (Krug 2001). Other ascoglossans including several Aplysia species (Switzer-Dunlap and Hadfield 1977; Switzer-Dunlap 1978) and *Placida* dendritica (Towbridge 1992) also settle in response to algae that



Fig. 7 *H. erythrogramma* larval settlement in response to bacteria isolated from the surface of **a** *C. officinalis* and **b** *A. anceps.* Data are mean percent settlement \pm SE, n = 5. *C* Strains from

constitute the preferred adult diet. For larvae such as these, the restricted diet of adults appears to be reflected in the restricted response of larvae to stimuli for settlement. Larvae will only settle when they locate the required adult habitat.

Our results indicate that bacterial biofilms, associated with a range of algae and non-living surfaces, are important for *H. erythrogramma* larval settlement. Interestingly, phylogenetically similar bacterial species

C. officinalis, A strains from A. anceps, Corallina C. officinalis, Amphiroa A. anceps

do not necessarily have the same effect on eukaryote larval settlement. Some bacteria within certain genera induce settlement of *H. erythrogramma*, while others from the same genera had no effect. Perhaps some bacteria within these groups are capable of producing biologically active metabolites, while others are not. Larvae of the polychaete *Hydroides elegans* also show both high and low settlement to various bacterial isolates (Unabia and Hadfield 1999) and strains

 Table 2
 16S rDNA sequence analysis of isolates. H High inducer, L low inducer

Alt D0008883 Aestariibacter halophilus 94.9 A130111 H C115 D0008803 Alfenormans sp. 96.7 A180191 H C229 D0008803 Marine gammaproteobacterium 96.7 A180191 H C230 D000885 Marine gammaproteobacterium 95.9 A1802050 H C36 D0008853 Marine gammaproteobacterium sp. 93.1 AY147861 H C46 D0008858 Protobacterium sp. 93.1 AY147861 H C416 D0008867 Protobacterium sp. 93.1 AY147861 H C416 D0008878 Preudoalterromonas heterolytica 97.9 X8128 H C416 D000887 Preudoalterromonas futoroidacea 99.4 X8214 H A13 D000886 Preudoalterromonas sp. 99.6 A391204 H A212 D0008864 Preudoalterromonas sp. 99.1 U80834 H A321 D0008877 Preudoalterromonas sp. 97.2	Isolate ^a	Accession number	BLAST closest match	Percentage of similarity	Accession number of closest match	Inducer
C115 DQ005870 Alphaproteobacteria 94.5 AF365994 H A232 DQ005879 Cytophage sp. 95.9 AB0735867 H C237 DQ005899 Cytophage sp. 95.9 AB0735867 H C36 DQ005883 Marine gammaproteobacterium sp. 97.3 AV582934 H C16 DQ005883 Photobacterium sp. 97.3 AV582934 H C16 DQ005888 Pseudoalteromonas hacterolytica 94.2 AF173902. H A340 DQ005888 Pseudoalteromonas durinficans 97.7 X82138 H C39 DQ005888 Pseudoalteromonas durinficans 97.9 X82138 H A131 DQ005884 Pseudoalteromonas sp. 98.6 A1391204 H A213 DQ005884 Pseudoalteromonas sp. 99.6 A1391204 H A213 DQ005871 Pseudoalteromonas sp. 97.2 A187451 H A214 DQ005871 Pseudoalteromonas sp. 97.2 A1	A14	DQ005853	Aestuariibacter halophilus	94.9	AJ391191	Н
A323 DQ005873 Alteronionas sp. 96.7 A130191 H C229 DQ005903 Marine gammaproteobacterium 96.8 AF360500 H C36 DQ005883 Micrococcus sp. 95.9 AV258119 H A137 DQ005883 Photobacterium sp. 93.1 AV147861 H C419 DQ005883 Photobacterium sp. 97 AJ842344 H A360 DQ005888 Pseudoalteromonas haterolytica 94.2 AF173962 H A41 DQ005888 Pseudoalteromonas haterolytica 99.4 X82138 H A313 DQ005884 Pseudoalteromonas theoviolacea 99.4 X8214 H A22 DQ005884 Pseudoalteromonas sp. 99.6 AJ37131 H A213 DQ005884 Pseudoalteromonas sp. 99.1 U80834 H A221 DQ005886 Pseudoalteromonas sp. 97.2 AJ37451 H A235 DQ005871 Pseudoalteromonas sp. 97.2 AJ374511 </td <td>C115</td> <td>DQ005890</td> <td>Alphaproteobacteria</td> <td>94.5</td> <td>AF365994</td> <td>Н</td>	C115	DQ005890	Alphaproteobacteria	94.5	AF365994	Н
C239 DQ005899 Cytophage sp. 95.9 AB075867 H C267 DQ005803 Marine gammaprotobacterium 96.8 AF3560450 H C36 DQ005883 Photobacterium sp. 97.3 AY582934 H C16 DQ005883 Photobacterium sp. 97.3 AY187861 H C419 DQ005878 Pseudoalteromonas bacterolytica 94.2 AF173962. H A340 DQ005878 Pseudoalteromonas bacterolytica 97.7 X82138 H C39 DQ005888 Pseudoalteromonas bacterolytica 97.9 X82138 H A316 DQ005884 Pseudoalteromonas spicevilaca 97.9 X82138 H A313 DQ005884 Pseudoalteromonas spice 99.4 X3131 H A315 DQ005884 Pseudoalteromonas spice 97.2 A1874511 H A325 DQ005871 Pseudoalteromonas spice 97.2 A1874511 H C17 DQ005871 Pseudoalteromonas spice 97.2 <td>A323</td> <td>DQ005873</td> <td>Alteromonas sp.</td> <td>96.7</td> <td>AJ391191</td> <td>Н</td>	A323	DQ005873	Alteromonas sp.	96.7	AJ391191	Н
C327 DQ005903 Marine gammaproteobacterium 96.8 AF36050 H C36 DQ005885 Micrococcus sp. 97.3 AY258119 H A137 DQ0058863 Photobacterium sp. 97.3 AY147861 H C419 DQ005906 Photobacterium sp. 97. AJ842344 H C419 DQ005878 Pseudoalterromonas hacterolytica 94.2 AF173962 H A360 DQ005858 Pseudoalterromonas hacterolytica 97.2 X82138 H A316 DQ005856 Pseudoalterromonas detaivrilocus 97.9 X82134 H A313 DQ005856 Pseudoalterromonas sp. 98.6 AV217773 H A321 DQ005856 Pseudoalterromonas sp. 98.1 U89854 H A321 DQ005871 Pseudoalterromonas sp. 97.1 U89854 H A321 DQ005871 Pseudoalterromonas sp. 97.2 AF80211 H A325 DQ005871 Pseudoalteromonas sp. 97.3	C239	DQ005899	Cytophaga sp.	95.9	ABO73567	Н
C36 D0008885 Micrococcus sp. 96.9 AY28291 H A137 D000883 Photobacterium sp. 97.3 AY58294 H C16 D0008883 Photobacterium sp. 97.4 AN42344 H A360 D0008578 Pseudoalteromonas hacterolytica 94.2 AP173962 H A341 D0008587 Pseudoalteromonas hacterolytica 97.7 X82188 H A316 D0008587 Pseudoalteromonas detairificans 97.9 X82144 H A315 D00085867 Pseudoalteromonas sp. 99.4 X82143 H A213 D00085861 Pseudoalteromonas sp. 98.7 AJ874351 H A213 D0008587 Pseudoalteromonas sp. 99.6 AJ874351 H A315 D0008587 Pseudoalteromonas sp. 97.2 AJ874351 H A317 D0008587 Pseudoalteromonas sp. 97.2 AJ874351 H A316 D0008587 Pseudoalteromonas sp. 97.2 AJ8	C327	DQ005903	Marine gammaproteobacterium	96.8	AF366050	Н
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C16 D0005883 Photobacterium sp. 93.1 AY1761 H C419 D0005976 Photobacterium sp. 97 AJ84234 H A360 D0005878 Pseudoalteromonas bacterolytica 94.2 AF173962 H A316 D0005888 Pseudoalteromonas denitrificans 97.9 X82144 H A316 D0005852 Pseudoalteromona sp. 99.4 X82144 H A213 D0005864 Pseudoalteromona sp. 99.6 AJ871351 H A213 D0005866 Pseudoalteromona sp. 99.7 AJ874351 H A214 D0005877 Pseudoalteromonas sp. 96.7 AJ874351 H A315 D0005877 Pseudoalteromonas sp. 97.2 AJ874351 H C127 D0005891 Pseudoalteromonas sp. 97.2 AJ874351 H C123 D0005891 Pseudoalteromonas sp. 97.2 AJ874351 H C123 D0005899 Pseudoalteromonas sp. 97.2 AJ874521<	A137	DQ005863	Photobacterium sp.	97.3	AY582934	Н
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C345D0005904Pseudoalteromonas sp.97.2AR\$30211HC127D0005892Pseudomonas sp.97.3AF\$00211HC123D0005898Pseudomonas sp.97.2AF\$00211HC123D0005891Pseudomonas stutzeri97.2AY125329HA367D0005891Pseudomonas stutzeri97.3AF145921HC111D0005889Shewanella sp.97.3AF145921HC136D0005894Shewanella sp.94.8AF145921HC377D0005868Shewanella waksmanii99AY170366HC357D0005882Thalassomonas viridans95.6A1294748HA510D0005889Vibrio mediterranei98.4X74710HA538D0005889Vibrio pomeroyi99.7AI491290HC319D0005893Algoriphagus winogradskyi96.6A1575263LC310D0005893Algoriphagus winogradskyi96.6A1575263LC47D0005886Gammaproteobacteria94.9AY207503LC47D0005886Gammaproteobacteria94.8AB008115LC212D0005907Pertinonas baleerica95.6A157263LC47D0005886Gammaproteobacteria96.9AY42344LA55D0005886Pseudoalteromonas sp.96.3AY26830LC312D0005907Pseudoalteromonas sp.96.3AY26830LC32 </td <td>A359</td> <td>DQ005877</td> <td>Pseudoalteromonas sp.</td> <td>94.7</td> <td>AY626830</td> <td>Н</td>	A359	DQ005877	Pseudoalteromonas sp.	94.7	AY626830	Н
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$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	C235	DQ005898	Pseudomonas sp.	97.2	AFS00211	Н
A367 DQ005879 Shewanella sp. 97.0 AF145921 H C111 DQ005894 Shewanella sp. 97.3 AF145921 H A317 DQ005868 Shewanella sp. 94.8 AF145921 H A317 DQ005868 Shewanella waksmanii 99 AY170366 H C357 DQ00582 Thalassomonas viridans 95.6 A1294748 H A318 DQ005882 Thalassomonas viridans 95.6 A1294748 H A338 DQ005889 Vibrio pomeroyi 99.7 AJ491290 H A538 DQ005880 Vibrio pomeroyi 99.7 AJ491290 H C130 DQ005893 Algoriphagus winogradskyi 96.6 A1575263 L C512 DQ005907 Ferrimonas balaerica 93.6 X93021 L C47 DQ00586 Marine bacteria 96.0 AY207503 L C218 DQ005881 Paraoccus sp. 94.8 AB008115 L <	C123	DQ005891	Pseudomonas stutzeri	97.2	AY125329	Н
C111DQ005889Shewanella sp.97.3AF145921HC136DQ005894Shewanella sp.94.8AF145921HC136DQ005868Shewanella waksmanii99AY170366HC357DQ005805Shewanella waksmanii95.0AY170366HA510DQ005882Thalassomonas viidans95.6AJ294748HA513DQ005869Vibrio mediterranei98.4X74710HA53DQ00589Vibrio pomeroyi99.7AJ491290HA358DQ005893Algoriphagus winogradskyi96.6AJ55263LC130DQ005933Algoriphagus winogradskyi96.6AJ55263LC512DQ005907Ferrimonas balaerica93.6K30021LC47DQ005886Gammaproteobacteria94.9AY207503LC218DQ005891Paraoccus sp.94.8AB008115LC222DQ005800Pseudoalteromonas rubra96.9AJ842344LC312DQ005860Pseudoalteromonas sp.96.3AY207503LC322DQ005861Pseudoalteromonas sp.96.3AY20350LA55DQ005861Pseudoalteromonas sp.96.3AY26830LA58DQ005851Pseudoalteromonas sp.96.5DQ008594LC312DQ005851Pseudoalteromonas sp.96.5DQ008594LC32DQ005855Roseobacter sp.95.6AJ324234LC33 </td <td>A367</td> <td>DQ005879</td> <td>Shewanella sp.</td> <td>97.0</td> <td>AF145921</td> <td>Н</td>	A367	DQ005879	Shewanella sp.	97.0	AF145921	Н
C136DQ005894Shewanella sp.94.8AF145921HA317DQ005868Shewanella waksmanii99AY170366HA310DQ005905Shewanella waksmanii95.6AJ294748HA510DQ005882Thalassomonas viridans95.6AJ294748HA318DQ005869Vibrio mediterranei98.4X74710HA53DQ005859Vibrio pomeroyi99.7AJ491290HA358DQ005880Vibrio pomeroyi93.5AJ630103HC130DQ005901Alpripatoebacteria97.1AF186699LC512DQ005901Alpriproteobacteria93.6X93021LC47DQ005886Gammaproteobacteria94.9AY207503LC218DQ005896Marine bacteria96.9AJ842344LC220DQ005807Photobacterium eurosenbergi96.9AJ842344LC312DQ005800Pseudoalteromonas rubra96.9X82147LC312DQ005851Pseudoalteromonas sp.96.8AY626830LC312DQ005851Pseudoalteromonas sp.96.3AY228115LA58DQ005861Pseudoalteromonas sp.96.2AJ391197LC22DQ005851Pseudoalteromonas sp.96.2AJ391197LC33DQ005874Raugeria sp.96.5DQ008584LC310DQ005855Shewanella waksmanii97.3AY170366LC33	C111	DQ005889	Shewanella sp.	97.3	AF145921	Н
A317DQ005868Shewanella waksmanii99AY170366HC357DQ005905Shewanella waksmanii95.0AY170366HA510DQ005882Thalassomonas viridans95.6A1294748HA318DQ005869Vibrio mediterranei98.4X74710HA53DQ005889Vibrio pomeroyi99.7AJ491290HA358DQ005880Vibrio pomeroyi99.7AJ491290HC130DQ005893Algoriphagus winogradskyi96.6AJ575263LC319DQ005901Alphaproteobacteria97.1AF186699LC47DQ005886Gammaproteobacteria94.9AY207503LC47DQ005886Gammaproteobacteria96.0AY626827LC218DQ005897Photobacterium eurosenbergii96.9AJ842344LA55DQ005807Pseudoalteromonas denitrificans97.1X82138LC312DQ005800Pseudoalteromonas sp.96.8AY626830LA349DQ005851Pseudoalteromonas sp.96.9X82147LA54DQ005861Pseudoalteromonas sp.96.2AJ391197LC32DQ005881Pseudoalteromonas sp.96.2AJ391197LC33DQ005851Pseudoalteromonas sp.96.2AJ391197LC34DQ005865Shewanella waksmanii97.3AY170366LC33DQ005865Shewanella waksmanii97.3AY170366	C136	DQ005894	Shewanella sp.	94.8	AF145921	Н
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	A317	DQ005868	Shewanella waksmanii	99	AY170366	Н
A510 $DQ005882$ Thalassomonas viridans95.6AJ294748HA318 $DQ005869$ Vibrio mediterranei98.4X74710HA53 $DQ005859$ Vibrio pomeroyi99.7AJ491290HA358 $DQ005880$ Vibrio ponticus93.5AJ630103HC130 $DQ005893$ Algoriphagus winogradskyi96.6AJ575263LC319 $DQ005907$ Ferrimonas balaerica93.6X93021LC47 $DQ005866$ Gammaproteobacteria94.9AY207503LC218 $DQ005886$ Gammaproteobacteria94.9AY207503LC218 $DQ0058861$ Paracoccus sp.94.8AB008115LC222 $DQ005887$ Photobacterium eurosenbergii96.9AJ842344LC312 $DQ005880$ Pseudoalteromonas rubra96.9X82147LC312 $DQ005851$ Pseudoalteromonas sp.96.8AY626830LA349 $DQ005875$ Pseudoalteromonas sp.96.2AJ391197LC23 $DQ005874$ Reugeria sp.96.2AJ391197LC23 $DQ005865$ Shewanella waksmanii97.3AY170366LC311 $DQ005865$ Shewanella waksmanii97.3AY170366LC32 $DQ005876$ Vibrio pomeroyi96.3AJ4170366LC33 $DQ005876$ Vibrio narveyi97.3AY170366LC34 $DQ005876$ Vibrio narveyi97.3AY170366 </td <td>C357</td> <td>DO005905</td> <td>Shewanella waksmanii</td> <td>95.0</td> <td>AY170366</td> <td>Н</td>	C357	DO005905	Shewanella waksmanii	95.0	AY170366	Н
A318 DQ005869 Vibrio mediterranei 98.4 X74710 H A53 DQ005859 Vibrio pomeroyi 99.7 AJ491290 H A358 DQ005880 Vibrio ponticus 93.5 AJ630103 H C130 DQ005893 Algoriphagus winogradskyi 96.6 AJ575263 L C319 DQ005901 Alphaproteobacteria 97.1 AF186699 L C512 DQ005886 Gammaproteobacteria 94.9 AY207503 L C47 DQ005886 Marine bacteria 96.0 AY2626827 L A510 DQ005886 Marine bacteria 96.0 AY207503 L C222 DQ005887 Photobacterium eurosenbergii 96.9 AJ842344 L A55 DQ005860 Pseudoalteromonas enlirificans 97.1 X82138 L C312 DQ005886 Pseudoalteromonas sp. 96.8 AY626830 L A349 DQ005875 Pseudoalteromonas sp. 96.3 AY258115 L A55 DQ005861 Pseudoalteromonas sp. 96.2 <td< td=""><td>A510</td><td>DQ005882</td><td>Thalassomonas viridans</td><td>95.6</td><td>AJ294748</td><td>Н</td></td<>	A510	DQ005882	Thalassomonas viridans	95.6	AJ294748	Н
A53 DQ005859 Vibrio pomeroyi 99.7 AJ491290 H A358 DQ005880 Vibrio ponticus 93.5 AJ630103 H C130 DQ005893 Algoriphagus winogradskyi 96.6 AJ575263 L C319 DQ005901 Alphaproteobacteria 97.1 AF186699 L C512 DQ005896 Gammaproteobacteria 94.9 AY207503 L C47 DQ005886 Gammaproteobacteria 96.0 AY626827 L A510 DQ005896 Marine bacteria 96.0 AY626827 L A510 DQ005881 Paracoccus sp. 94.8 AB008115 L C222 DQ005807 Photobacterium eurosenbergii 96.9 AJ842344 L A55 DQ005860 Pseudoalteromonas sp. 96.8 AY626830 L A25 DQ005851 Pseudoalteromonas sp. 96.8 AY626830 L A349 DQ005861 Pseudoalteromonas sp. 96.2 AJ391197 L C23 DQ005884 Roseobacter sp. 96.5 DQ008594	A318	DQ005869	Vibrio mediterranei	98.4	X74710	Н
A358 $D_{0005880}$ Vibrio ponticus93.5AJ630103HC130 $D_{0005893}$ Algoriphagus winogradskyi96.6AJ575263LC319 $D_{0005901}$ Alphaproteobacteria97.1AF186699LC512 $D_{0005907}$ Ferrimonas balaerica93.6X93021LC47 $D_{0005886}$ Gammaproteobacteria94.9AY207503LC218 $D_{0005881}$ Paracoccus sp.94.8AB008115LC222 $D_{0005897}$ Photobacterium eurosenbergii96.9AJ842344LA55 $D_{0005860}$ Pseudoalteromonas denitrificans97.1X82138LC312 $D_{0005807}$ Pseudoalteromonas rubra96.9X82147LA25 $D_{0005875}$ Pseudoalteromonas sp.96.8AY626830LA349 D_{005875} Pseudoalteromonas sp.96.3AY258115LA333 $D_{0005874}$ Reugeria sp.96.5D0005894LC216 $D_{0005895}$ Roseobacter sp.95.6AJ334238LA311 $D_{0005862}$ Shewanella waksmanii97.3AY170366LA352 $D_{0005876}$ Vibrio pomeroyi96.3AJ491290LA352 $D_{0005876}$ Vibrio narveyi97.3AY967728LC312 $D_{0005876}$ Vibrio narveyi97.3AJ910366LC321 $D_{0005876}$ Vibrio pomeroyi96.3AJ491290LC33 $D_{0005876}$	A53	DO005859	Vibrio pomerovi	99.7	AJ491290	Н
C130 DQ005893 Algoriphagus winogradskyi 96.6 AJ575263 L C319 DQ005901 Alphaproteobacteria 97.1 AF186699 L C512 DQ005886 Gammaproteobacteria 93.6 X93021 L C47 DQ005886 Gammaproteobacteria 94.9 AY207503 L C218 DQ005881 Paracoccus sp. 94.8 AB008115 L C222 DQ005887 Photobacterium eurosenbergii 96.9 AJ842344 L A55 DQ005860 Pseudoalteromonas denitrificans 97.1 X82138 L C312 DQ005851 Pseudoalteromonas sp. 96.8 AY626830 L A25 DQ005875 Pseudoalteromonas sp. 96.3 AY258115 L A349 DQ005874 Reugeria sp. 96.2 AJ391197 L C23 DQ005884 Roseobacter sp. 96.5 DQ008594 L C311 DQ005885 Shewanella waksmanii 97.3 AY170366 L	A358	DQ005880	Vibrio ponticus	93.5	AJ630103	Н
C319DQ005901Alphaproteobacteria97.1AF186699LC512DQ005907Ferrimonas balaerica93.6X93021LC47DQ005886Gammaproteobacteria94.9A Y207503LC218DQ005896Marine bacteria96.0AY626827LA510DQ005881Paracoccus sp.94.8AB008115LC222DQ005887Photobacterium eurosenbergii96.9AJ842344LA55DQ005860Pseudoalteromonas denitrificans97.1X82188LC312DQ005801Pseudoalteromonas rubra96.9X82147LA25DQ005851Pseudoalteromonas sp.96.8AY626830LA349DQ005875Pseudoalteromonas sp.96.3AY258115LA58DQ005861Pseudoalteromonas sp.96.2AJ391197LC23DQ005874Reugeria sp.96.2AJ534238LC216DQ005855Roseobacter sp.95.6AJ534238LC311DQ005862Silicibacter lacuscaerulensis98.9U77644LA356DQ005876Vibrio harveyi97.3AY170366LC32DQ005876Vibrio pomeroyi96.3AJ491290LC33DQ005876Vibrio polendidus95.2AJ80386LA322DQ005875Vibrio splendidus96.3AJ491290LA32DQ005872Vibrio splendidus95.2AJ84361LA32 <td>C130</td> <td>DQ005893</td> <td>Algoriphagus winogradskyi</td> <td>96.6</td> <td>AJ575263</td> <td>L</td>	C130	DQ005893	Algoriphagus winogradskyi	96.6	AJ575263	L
C512 DQ005907 Ferrimonas balaerica 93.6 X93021 L C47 DQ005886 Gammaproteobacteria 94.9 AY207503 L C218 DQ005886 Marine bacteria 96.0 AY626827 L A510 DQ005881 Paracoccus sp. 94.8 AB008115 L C222 DQ005897 Photobacterium eurosenbergii 96.9 AJ842344 L A55 DQ005860 Pseudoalteromonas denitrificans 97.1 X82138 L C312 DQ005851 Pseudoalteromonas sp. 96.8 AY626830 L A255 DQ005851 Pseudoalteromonas sp. 96.3 AY258115 L A25 DQ005851 Pseudoalteromonas sp. 96.2 AJ391197 L C33 DQ005874 Reugeria sp. 96.2 AJ391197 L C23 DQ005884 Roseobacter sp. 95.6 AJ534238 L A311 DQ005865 Shewanella waksmanii 97.3 AY170366 L	C319	DQ005901	Alphaproteobacteria	97.1	AF186699	L
C47 $D_{0005886}$ Gammaproteobacteria94.9 $AY207503$ LC218 $DQ005896$ Marine bacteria96.0 $AY626827$ LA510 $DQ005881$ Paracoccus sp.94.8 $AB008115$ LC222 $DQ005897$ Photobacterium eurosenbergii96.9 $AI842344$ LA55 $DQ005860$ Pseudoalteromonas denitrificans97.1 $X82138$ LC312 $DQ005851$ Pseudoalteromonas rubra96.9 $X82147$ LA25 $DQ005851$ Pseudoalteromonas sp.96.8 $AY626830$ LA349 $DQ005875$ Pseudoalteromonas sp.96.2 $AY626830$ LA333 $DQ005874$ Reugeria sp.96.2 $AY626830$ LC23 $DQ005895$ Roseobacter sp.96.2 $AJ391197$ LC216 $DQ005895$ Roseobacter sp.95.6 $AJ534238$ LC311 $DQ005865$ Shewanella waksmanii99.3 $AY170366$ LC321 $DQ005876$ Vibrio harveyi97.3 $AY967728$ LC33 $DQ005876$ Vibrio pomeroyi96.3 $AI491290$ LA356 $DQ005876$ Vibrio pomeroyi96.3 $AI491290$ LA322 $DQ005872$ Vibrio splendidus96.9 $AY620972$ LA310 $DQ005875$ Vibrio splendidus95.2 $AI874361$ LA311 $DQ005875$ Vibrio splendidus95.2 $AI874361$ LA311 $DQ005875$ Vibrio splendidus<	C512	DQ005907	Ferrimonas balaerica	93.6	X93021	L
C218 $DQ005896$ Marine bacteria96.0AY626827LA510 $DQ005881$ Paracoccus sp.94.8AB008115LC222 $DQ005897$ Photobacterium eurosenbergii96.9AJ842344LA55 $DQ005860$ Pseudoalteromonas denitrificans97.1X82138LC312 $DQ005900$ Pseudoalteromonas rubra96.9X82147LA25 $DQ005851$ Pseudoalteromonas sp.96.8AY626830LA349 $DQ005875$ Pseudoalteromonas sp.96.3AY258115LA58 $DQ005861$ Pseudoalteromonas sp.98.2AY626830LA333 $DQ005874$ Reugeria sp.96.2AJ391197LC23 $DQ005884$ Roseobacter sp.95.6AJ534238LC216 $DQ005895$ Roseobacter sp.95.6AJ534238LC321 $DQ005865$ Shewanella waksmanii99.3AY170366LA115 $DQ005862$ Silicibacter lacuscaerulensis98.9U77644LA356 $DQ005876$ Vibrio pomeroyi97.3AY967728LA322 $DQ005876$ Vibrio splendidus96.9AY620972LA310 $DQ005875$ Vibrio splendidus95.2AJ874361LA311 $DQ005855$ Vibrio splendidus95.2AJ874361LA31 $DQ005855$ Vibrio splendidus95.2AJ874361L	C47	DQ005886	Gammaproteobacteria	94.9	AY207503	L
A510 DQ005881 Paracoccus sp. 94.8 AB008115 L C222 DQ005897 Photobacterium eurosenbergii 96.9 AJ842344 L A55 DQ005860 Pseudoalteromonas denitrificans 97.1 X82138 L C312 DQ005900 Pseudoalteromonas rubra 96.9 X82147 L A25 DQ005851 Pseudoalteromonas sp. 96.8 AY626830 L A349 DQ005875 Pseudoalteromonas sp. 96.3 AY258115 L A58 DQ005874 Reugeria sp. 96.2 AJ391197 L C23 DQ005874 Reugeria sp. 96.5 DQ008594 L C216 DQ005865 Shewanella waksmanii 99.3 AY170366 L C321 DQ005862 Silicibacter lacuscaerulensis 98.9 U77644 L C321 DQ005876 Vibrio harveyi 97.3 AY967728 L C33 DQ005876 Vibrio pomeroyi 96.3 AJ491290 L C33 DQ005876 Vibrio splendidus 96.9 AY620972 </td <td>C218</td> <td>DQ005896</td> <td>Marine bacteria</td> <td>96.0</td> <td>AY626827</td> <td>L</td>	C218	DQ005896	Marine bacteria	96.0	AY626827	L
C222 DQ005897 Photobacterium eurosenbergii 96.9 AJ842344 L A55 DQ005860 Pseudoalteromonas denitrificans 97.1 X82138 L C312 DQ005900 Pseudoalteromonas rubra 96.9 X82147 L A25 DQ005851 Pseudoalteromonas sp. 96.8 AY626830 L A349 DQ005875 Pseudoalteromonas sp. 96.3 AY258115 L A58 DQ005861 Pseudoalteromonas sp. 96.2 AJ391197 L C23 DQ005874 Reugeria sp. 96.5 DQ008594 L C216 DQ005885 Roseobacter sp. 95.6 AJ534238 L C311 DQ005865 Shewanella waksmanii 99.3 AY170366 L C321 DQ005876 Vibrio harveyi 97.3 AY967728 L C321 DQ005876 Vibrio nopmeroyi 96.3 AJ491290 L A356 DQ005876 Vibrio splendidus 96.9 AY620972 L	A510	DQ005881	Paracoccus sp.	94.8	AB008115	L
A55DQ005860Pseudoalteromonas denitrificans97.1X82138LC312DQ005900Pseudoalteromonas rubra96.9X82147LA25DQ005851Pseudoalteromonas sp.96.8AY626830LA349DQ005875Pseudoalteromonas sp.96.3AY258115LA58DQ005861Pseudoalteromonas sp.98.2AY626830LA333DQ005874Reugeria sp.96.2AJ391197LC23DQ005884Roseobacter sp.96.5DQ008594LC216DQ005865Shewanella waksmanii99.3AY170366LC311DQ005865Shewanella waksmanii97.3AY170366LC312DQ005862Silicibacter lacuscaerulensis98.9U77644LA356DQ005876Vibrio harveyi97.3AY967728LC53DQ005856Vibrio pomeroyi96.3AJ491290LA322DQ005872Vibrio splendidus96.9AY620972LA319DQ005870Vibrio splendidus95.2AJ874361LA31DQ005855Vibrio splendidus95.2AJ874361L	C222	DQ005897	Photobacterium eurosenbergii	96.9	AJ842344	L
C312 DQ005900 Pseudoalteromonas rubra 96.9 X82147 L A25 DQ005851 Pseudoalteromonas sp. 96.8 AY626830 L A349 DQ005875 Pseudoalteromonas sp. 96.3 AY258115 L A58 DQ005861 Pseudoalteromonas sp. 98.2 AY626830 L A333 DQ005874 Reugeria sp. 96.2 AJ391197 L C23 DQ005884 Roseobacter sp. 96.5 DQ008594 L C216 DQ005865 Shewanella waksmanii 99.3 AY170366 L C311 DQ005865 Shewanella waksmanii 97.3 AY170366 L C321 DQ005862 Silicibacter lacuscaerulensis 98.9 U77644 L A356 DQ005876 Vibrio pomeroyi 97.3 AY967728 L C432 DQ005876 Vibrio opmeroyi 96.3 AJ491290 L A320 DQ005872 Vibrio splendidus 96.9 AY620972 L <td>A55</td> <td>DQ005860</td> <td>Pseudoalteromonas denitrificans</td> <td>97.1</td> <td>X82138</td> <td>L</td>	A55	DQ005860	Pseudoalteromonas denitrificans	97.1	X82138	L
A25DQ005851Pseudoalteromonas sp.96.8AY626830LA349DQ005875Pseudoalteromonas sp.96.3AY258115LA58DQ005861Pseudoalteromonas sp.98.2AY626830LA333DQ005874Reugeria sp.96.2AJ391197LC23DQ005884Roseobacter sp.96.5DQ008594LC216DQ005895Roseobacter sp.95.6AJ534238LA311DQ005865Shewanella waksmanii99.3AY170366LC321DQ005862Silicibacter lacuscaerulensis98.9U77644LA356DQ005876Vibrio harveyi97.3AY967728LC53DQ005887Vibrio pomeroyi96.3AJ491290LA322DQ005876Vibrio sp.99.7AB180386LA319DQ005870Vibrio splendidus96.9AY620972LA31DQ005855Vibrio sp.99.3AJ845021L	C312	DQ005900	Pseudoalteromonas rubra	96.9	X82147	L
A349DQ005875Pseudoalteromonas sp.96.3AY258115LA58DQ005861Pseudoalteromonas sp.98.2AY626830LA333DQ005874Reugeria sp.96.2AJ391197LC23DQ005884Roseobacter sp.96.5DQ008594LC216DQ005895Roseobacter sp.95.6AJ534238LA311DQ005865Shewanella waksmanii99.3AY170366LC321DQ005862Silicibacter lacuscaerulensis98.9U77644LA356DQ005876Vibrio harveyi97.3AY967728LC53DQ005887Vibrio sp.99.7AB180386LA322DQ005872Vibrio splendidus96.9AY620972LA319DQ005870Vibrio splendidus95.2AJ874361LA31DQ005855Vibrio sp.99.3AJ845021L	A25	DQ005851	Pseudoalteromonas sp.	96.8	AY626830	L
A58DQ005861Pseudoalteromonas sp.98.2AY626830LA333DQ005874Reugeria sp.96.2AJ391197LC23DQ005884Roseobacter sp.96.5DQ008594LC216DQ005895Roseobacter sp.95.6AJ534238LA311DQ005865Shewanella waksmanii99.3AY170366LC321DQ005902Shewanella waksmanii97.3AY170366LA115DQ005862Silicibacter lacuscaerulensis98.9U77644LA356DQ005876Vibrio harveyi97.3AY967728LC53DQ005887Vibrio sp.99.7AB180386LA322DQ005872Vibrio splendidus96.9AY620972LA319DQ005870Vibrio splendidus95.2AJ874361LA31DQ005855Vibrio sp.99.3AJ845021L	A349	DQ005875	Pseudoalteromonas sp.	96.3	AY258115	L
A333DQ005874Reugeria sp.96.2AJ391197LC23DQ005884Roseobacter sp.96.5DQ008594LC216DQ005895Roseobacter sp.95.6AJ534238LA311DQ005865Shewanella waksmanii99.3AY170366LC321DQ005902Shewanella waksmanii97.3AY170366LA115DQ005862Silicibacter lacuscaerulensis98.9U77644LA356DQ005876Vibrio harveyi97.3AY967728LC53DQ005887Vibrio pomeroyi96.3AJ491290LA322DQ005856Vibrio sp.99.7AB180386LA319DQ005870Vibrio splendidus95.2AJ874361LA31DQ005855Vibrio sp.99.3AJ845021L	A58	DQ005861	Pseudoalteromonas sp.	98.2	AY626830	L
C23 DQ005884 Roseobacter sp. 96.5 DQ008594 L C216 DQ005895 Roseobacter sp. 95.6 AJ534238 L A311 DQ005865 Shewanella waksmanii 99.3 AY170366 L C321 DQ005902 Shewanella waksmanii 97.3 AY170366 L A115 DQ005862 Silicibacter lacuscaerulensis 98.9 U77644 L A356 DQ005876 Vibrio harveyi 97.3 AY967728 L C53 DQ005887 Vibrio pomeroyi 96.3 AJ491290 L A322 DQ005876 Vibrio sp. 99.7 AB180386 L A322 DQ005872 Vibrio splendidus 96.9 AY620972 L A319 DQ005870 Vibrio splendidus 95.2 AJ874361 L A31 DQ005855 Vibrio sp. 99.3 AJ845021 L	A333	DO005874	Reugeria sp.	96.2	AJ391197	L
C216 DQ005895 Roseobacter sp. 95.6 AJ534238 L A311 DQ005865 Shewanella waksmanii 99.3 AY170366 L C321 DQ005902 Shewanella waksmanii 97.3 AY170366 L A115 DQ005862 Silicibacter lacuscaerulensis 98.9 U77644 L A356 DQ005876 Vibrio harveyi 97.3 AY967728 L C53 DQ005887 Vibrio pomeroyi 96.3 AJ491290 L A322 DQ005872 Vibrio splendidus 96.9 AY620972 L A319 DQ005870 Vibrio splendidus 95.2 AJ874361 L A31 DQ005855 Vibrio sp. 99.3 AJ845021 L	C23	DO005884	Roseobacter sp.	96.5	DO008594	L
A311DQ005865Shewanella waksmanii99.3AY170366LC321DQ005902Shewanella waksmanii97.3AY170366LA115DQ005862Silicibacter lacuscaerulensis98.9U77644LA356DQ005876Vibrio harveyi97.3AY967728LC53DQ005887Vibrio pomeroyi96.3AJ491290LA32DQ005856Vibrio sp.99.7AB180386LA322DQ005872Vibrio splendidus96.9AY620972LA319DQ005870Vibrio splendidus95.2AJ874361LA31DQ005855Vibrio sp.99.3AJ845021L	C216	DO005895	Roseobacter sp.	95.6	AJ534238	L
C321 DQ005902 Shewanella waksmanii 97.3 AY170366 L A115 DQ005862 Silicibacter lacuscaerulensis 98.9 U77644 L A356 DQ005876 Vibrio harveyi 97.3 AY967728 L C53 DQ005887 Vibrio pomeroyi 96.3 AJ491290 L A322 DQ005876 Vibrio sp. 99.7 AB180386 L A322 DQ005872 Vibrio splendidus 96.9 AY620972 L A319 DQ005870 Vibrio splendidus 95.2 AJ874361 L A31 DQ005855 Vibrio sp. 99.3 AJ845021 L	A311	DO005865	Shewanella waksmanii	99.3	AY170366	L
A115 DQ005862 Silicibacter lacuscaerulensis 98.9 U77644 L A356 DQ005876 Vibrio harveyi 97.3 AY967728 L C53 DQ005887 Vibrio pomeroyi 96.3 AJ491290 L A32 DQ005856 Vibrio sp. 99.7 AB180386 L A322 DQ005872 Vibrio splendidus 96.9 AY620972 L A319 DQ005855 Vibrio sp. 95.2 AJ874361 L A31 DQ005855 Vibrio sp. 99.3 AJ845021 L	C321	DQ005902	Shewanella waksmanii	97.3	AY170366	L
A356 DQ005876 Vibrio harveyi 97.3 AY967728 L C53 DQ005887 Vibrio pomeroyi 96.3 AJ491290 L A32 DQ005856 Vibrio sp. 99.7 AB180386 L A322 DQ005872 Vibrio splendidus 96.9 AY620972 L A319 DQ005855 Vibrio spl. 95.2 AJ874361 L A31 DQ005855 Vibrio sp. 99.3 AJ845021 L	A115	DQ005862	Silicibacter lacuscaerulensis	98.9	U77644	L
Child Control Control <thcontrol< th=""> <thcontrol< th=""> <thcon< td=""><td>A356</td><td>DO005876</td><td>Vibrio harvevi</td><td>97.3</td><td>AY967728</td><td>Ē</td></thcon<></thcontrol<></thcontrol<>	A356	DO005876	Vibrio harvevi	97.3	AY967728	Ē
A32 DQ005856 Vibrio sp. 99.7 AB180386 L A322 DQ005872 Vibrio splendidus 96.9 AY620972 L A319 DQ005855 Vibrio spl. 95.2 AJ874361 L A31 DQ005855 Vibrio sp. 99.3 AJ845021 L	C53	DO005887	Vibrio pomerovi	96.3	AJ491290	Ē
A322 DQ005872 Vibrio splendidus 96.9 AY620972 L A319 DQ005850 Vibrio splendidus 95.2 AJ874361 L A31 DQ005855 Vibrio sp. 99.3 AJ845021 L	A32	DO005856	Vibrio sp.	99.7	AB180386	Ĺ
A319 DQ005870 Vibrio splendidus 95.2 AJ874361 L A31 DQ005855 Vibrio sp. 99.3 AJ845021 L	A 322	DO005872	Vibrio splendidus	96.9	AY620972	Ē.
A31 DQ005855 Vibrio sp. 99.3 AJ845021 L	A319	DO005870	Vibrio splendidus	95.2	A 1874361	Ē.
	A31	DQ005855	Vibrio sp.	99.3	AJ845021	Ľ

^a Codes for isolates are from Fig. 7 and remaining settlement assays

Fig. 8 *H. erythrogramma* settlement in traps in response to the high-inducing biofilm *Pseudoalteromonas luteoviolacea* (*H*), the unfilmed control (*C*), and the low-inducing biofilm *Pseudoalteromonas rubra* (*L*). Larvae were enclosed in traps. Data are mean percent settlement \pm SE, n = 10

inducing both responses have now been identified as belonging to the genera Pseudoalteromonas, Vibrio, and Alteromonas (Lau et al. 2002). These studies present evidence for a number of different bacteria inducing the same settlement response from a eukaryotic larva, suggesting a redundancy in the function of bacteria on the surface of coralline algae (this study) and on an artificial settlement surface (Unabia and Hadfield 1999; Lau et al. 2002). In both cases, there was not simply a single bacterial species that indicated a suitable settlement surface, but rather a diverse range each performing the same function. While a wide taxonomic range of bacteria induce settlement of these larvae, strains of P. luteoviolacea has now been identified as inducing a high settlement response for two species of invertebrates: H. elegans (Huang and Hadfield 2003) and H. erythrogramma (this study).

H. erythrogramma larvae, when enclosed in traps in the field, metamorphosed in significantly higher numbers on P. luteoviolacea than on either the low-inducing biofilm P. rubra or the unfilmed control. Raimondi and Morse (2000) were also able to demonstrate that the coral Agaricia humilis settles at various depths inside traps in the field in response to a chemical cue. To our knowledge, ours is the first field experiment to show that larvae are able to respond to a characterised bacterial biofilm in the field. Browne and Zimmer (2001) demonstrated that when larval traps emitting tracers of a waterborne peptide were deployed in an estuary, significantly more Balanus amphitrite larvae were able to successfully recruit in response to the presence of the peptide. For *H. erythrogramma* larvae, when larvae were released into the water column near traps, only a very small number of individuals were able to locate the inducing biofilm. One explanation is that local hydrodynamic conditions may have transported larvae away from traps. Alternatively larvae in traps may have been subject to heavy predation. Demonstrations of the effects of settlement inducers in the complex ecological and hydrodynamic environment of natural habitats remain a significant challenge for studies of settlement cues.

Bacteria that induced high rates of settlement of H. erythrogramma larvae were dominated by Gammaproteobacteria contributing to a growing body of work suggesting that Gammaproteobacteria are important as inducers of larval settlement. Pseudomonas A3 induces larval settlement of the coral larvae Acropora millepora and A. willisae (Negri et al. 2001), the scyphozoan larvae Cassiopea andromeda settle when exposed to Vibrio sp. (Hofmann and Brand 1987), and bacteria from the genus Alteromonas induce settlement of larvae of the hydrozoan Hydractinia echinata (reviewed by Leitz 1997). The fouling polychaete *H. elegans* also settles to a range of bacterial isolates dominated by Gammaproteobacteria (Lau et al. 2002), exopolymers produced by a marine *Pseudoalteromonas* strain enhance attachment of the ascidian Ciona intestinalis (Szewzyk et al. 1991) and Alteromonas colwelliana promotes settlement by larvae of the oyster Crassostrea gigas (Weiner et al. 1989). Gammaproteobacteria, particularly bacteria from the *Pseudoalteromonas*, are frequently isolated from eukaryotic hosts such as marine algae (reviewed by Holmström and Kjelleberg 1999) and are known to produce biologically active metabolites that mediate interactions such as antifungal (Barbieri et al. 2001), antifouling (Holmström et al. 1992; Holmström and Kjelleberg 2000) and antibacterial activity (Hentschel et al. 2001). Given their broad association with eukaryotic hosts in the marine environment, it is not surprising that these bacteria are important as mediators of settlement.

Most studies that have sought to investigate the importance of surface-associated bacteria to settlement of marine invertebrate larvae have focused only on the members of the bacterial community that are able to be cultured. Ours, and other recent studies, employ a more holistic approach through use of various molecular techniques (e.g. Webster et al. 2004; Lau et al. 2005). DGGE, a DNA fingerprinting method that compares microbial community diversity among samples, revealed that community composition of biofilms on plants is important for larval settlement of *H. erythrogramma*. Similarly, two species of barnacles, *B. amphitrite* and *Balanus trigonus*, also display differential settlement in response to changes in biofilm commu-

nity composition (Lau et al. 2005). Conversely, Webster et al. (2004) were unable to detect differences between coral reef biofilms that did and did not induce coral larval settlement. They concluded that differential coral settlement was due to changes of single bacterial species within biofilms which could not be detected using the techniques employed. Future development and application of these and other molecular techniques should substantially increase our understanding of important components of marine biofilms for larval settlement.

Settlement assays with larvae and surfaces treated with antibiotics can be challenging because of potential artefacts (Johnson and Sutton 1994). To control for the possible effect of antibiotics on algae, we tested the settlement response of larvae of the sea urchin H. purpurascens, which settles in response to histamine isolated from the host alga D. pulchra (Swanson et al. 2004), in the presence and absence of antibiotics. Both our study and Swanson et al. (2004) found that the application of antibiotics did not reduce the settlement response to D. pulchra by H. purpurascens larvae, suggesting that antibiotics do not affect the efficacy of this algal chemical cue. The application of antibiotics to two coralline algae saw a corresponding drop in *H. erythrogramma* larval settlement. This drop was not seen in the equivalent assays using H. purpurascens larvae, suggesting that different sources are responsible for the settlement cues of these co-occurring urchin species, and that the cue for settlement by H. erythrogramma larvae is not an algal chemical cue. We also tested the response of larvae that were reared in FSW containing antibiotics and larvae that were exposed to antibiotics during assays in comparison to controls. These experiments indicated that antibiotics did not have any visible effects on the larval settlement behaviour of H. erythrogramma.

Many larvae settle in response to coralline algae (reviewed by Roberts 2001). For Acanthaster planci larvae, no settlement occurs on either boiled or autoclaved CCA (Johnson et al. 1991b). However, neither mixed- nor single-strain biofilms of bacteria isolated from CCA induce settlement, initially suggesting that induction is not bacterially induced (Johnson et al. 1991b). Further experiments indicated that when bacteria were re-infected onto CCA previously treated with antibiotics, settlement was once again strongly induced (Johnson and Sutton 1994). Another interesting case is for larvae of the corals A. willisae and A. millepora (Negri et al. 2001). Both species settle in response to CCA; however this response is not reduced either through treatment of CCA with antibiotics, or by autoclaving. A single bacterium, isolated from CCA, was able to induce settlement, but only in the presence of *Porites* sp. (Negri et al. 2001). These studies suggest that bacteria isolated from CCA are important for larval settlement, but that compounds from a source of calcium carbonate, such as CCA, are also needed to provide a cue. This was not the case for *H. erythrogramma* larvae though, as single-strain biofilms grown on glass slides were able to induce rates of settlement as high as on coralline algae (Fig. 7).

While the DGGE analyses conducted here include changes in cyanobacteria, one aspect of biofilms that has not been specifically investigated in this study is the photosynthetic component. Changes to ephemeral algal cover by grazers can impact the composition of intertidal community assemblages (Anderson and Underwood 1997) and the availability of both bacteria and diatoms impacts the growth and success of intertidal grazing molluscs (Thompson et al. 2000). Furthermore, for a number of invertebrate larval species, both the bacterial and diatom components of biofilms are important for settlement (Harder et al. 2002; Lau et al. 2003; Dahms et al. 2004; Patil and Anil 2005), and the importance of diatoms for settlement of abalone larvae has been well documented (reviewed by Roberts 2001). While we have demonstrated the importance of bacteria in settlement of H. erythrogramma larvae, it remains possible that diatoms and unicellular algal species within mixed biofilm communities also influence larval settlement of this species.

Here we have addressed the hypothesis that larvae of generalist herbivores settle in response to broadly distributed settlement cues, such as bacterial biofilms. A wide range of algae and biofilmed (but otherwise non-living) surfaces all induced settlement of H. erythrogramma larvae, with coralline algae inducing settlement at the highest rates. Settlement was reduced when coralline algae were autoclaved and when they were treated with antibiotics. Antibiotic treatments caused a drop in the diversity of culturable bacteria and a shift in the microbial community diversity. A diverse range of bacteria isolated from coralline algae also induced settlement of larvae, both in the laboratory and in the field. The distribution of new recruits in the field confirms the settlement results obtained in the laboratory-recruitment predominantly occurs on coralline algae with small numbers of recruits also found on co-occurring algae and rubble (M. J. Huggett et al., in preparation). These results support the hypothesis that larvae are responding to biofilm cues, and that these biofilms are likely to be distributed across many algal species and biofilmed (but otherwise non-living) substrata. However, we have also addressed this hypothesis for larvae of the generalist herbivore H.

rubra (Huggett et al. 2005). In contrast to the results found here for *H. erythrogramma*, *H. rubra* larval settlement does not appear to be primarily driven by biofilm-based cues, despite displaying broad spectrum settlement to a range of macroalgae. The difference in the types of cues that are important for larval settlement of *H. rubra* and *H. erythrogramma* indicate that despite similarities in adult habitat use, generalist invertebrate herbivores do not all respond to the same type of cues, and in particular, that while bacterial biofilm cues are important for some generalist larvae, including *H. erythrogramma*, they are not necessarily a source of settlement cues for all generalists.

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